

SEQUENCE LISTING

<110> Institut National de la Santé et de la Recherche Médicale -
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<120> Method for demonstration of a molecular event in a cell by means of
fluorescent marker proteins

<130> D20600

<140> PCT/FR2004/001678
<141> 2004 - 06 - 30

<150> FR 03/08 186
<151> 2003-07-04

<160> 14

<170> PatentIn version 3.2

<210> 1
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<212> DNA
<213> Artificial sequence

<220>
<223> Probe

<220>
<221> CDS
<222> (1)..(174)

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Glu Gly Gly Gly Ser Asp Glu Val Asp Ser Gly Gly Gly Ser
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gga ggt ggc gga tcc ttc gag ccg tcc gaa act ctg atc act acc gtt 96
Gly Gly Gly Ser Phe Glu Pro Ser Glu Thr Leu Ile Thr Thr Val
20 25 30

gaa tcg aac tcg agt tgg tgg act aac tgg gtt atc cct gcg atc tct 144
Glu Ser Asn Ser Ser Trp Trp Thr Asn Trp Val Ile Pro Ala Ile Ser
35 40 45

gct ctg gtt gta gcg ctg atg tac cgg cgt taatgactgc agtctagagg g 195
Ala Leu Val Val Ala Leu Met Tyr Arg Arg
50 55

<210> 2
<211> 58
<212> PRT

213> Artificial sequence

<220>
<223> Probe

<400> 2

Glu Gly Gly Gly Ser Asp Glu Val Asp Ser Gly Gly Gly Ser
 1 5 10 15

Gly Gly Gly Ser Phe Glu Pro Ser Glu Thr Leu Ile Thr Thr Val
 20 25 30

Glu Ser Asn Ser Ser Trp Trp Thr Asn Trp Val Ile Pro Ala Ile Ser
 35 40 45

Ala Leu Val Val Ala Leu Met Tyr Arg Arg
 50 55

<210> 3
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<220>
 <223> Caspase 3 probe DEVD-SNAP-25 (80-136)

<220>
 <221> CDS
 <222> (1)...(291)

<400> 3

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1 5 10 15	

gga ggt ggc gga tcc ttc gag ccg tcc gaa act ctg atc act acc gtt	96
Gly Gly Gly Ser Phe Glu Pro Ser Glu Thr Leu Ile Thr Thr Val	
20 25 30	

gaa tcg aac tcg agt atg gac cta gga aaa ttc tgc ggg ctt tgt gtg	144
Glu Ser Asn Ser Ser Met Asp Leu Gly Lys Phe Cys Gly Leu Cys Val	
35 40 45	

tgt ccc tgt aac aag ctt aaa tcc agt gat gct tac aaa aaa gcc tgg	192
Cys Pro Cys Asn Lys Leu Lys Ser Ser Asp Ala Tyr Lys Lys Ala Trp	
50 55 60	

ggc aat aat cag gat gga gta gtg gcc agc cag cct gcc cgt gtg gtg	240
Gly Asn Asn Gln Asp Gly Val Val Ala Ser Gln Pro Ala Arg Val Val	
65 70 75 80	

gat gaa cgg gag cag atg gcc atc agt ggt ggc ttc atc cgc aga cgc	288
Asp Glu Arg Glu Gln Met Ala Ile Ser Gly Gly Phe Ile Arg Arg Arg	
85 90 95	

gtc taa
 Val

<210> 4

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 <213> Artificial sequence

<220>
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<400> 4.

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Gly Gly Gly Ser Phe Glu Pro Ser Glu Thr Leu Ile Thr Thr Val
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Glu Ser Asn Ser Ser Met Asp Leu Gly Lys Phe Cys Gly Leu Cys Val
 35 40 45

Cys Pro Cys Asn Lys Leu Lys Ser Ser Asp Ala Tyr Lys Lys Ala Trp
 50 55 60

Gly Asn Asn Gln Asp Gly Val Val Ala Ser Gln Pro Ala Arg Val Val
 65 70 75 80

Asp Glu Arg Glu Gln Met Ala Ile Ser Gly Gly Phe Ile Arg Arg Arg
 85 90 95

Val

<210> 5
 <211> 294
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Caspase 8 probe IETD SNAP-25 (80-136)

<220>
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 <222> (1)..(291)

<400> 5
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 1 5 10 15

gga ggt ggc gga tcc ttc gag ccg tcc gaa act ctg atc act acc gtt 96
 Gly Gly Gly Ser Phe Glu Pro Ser Glu Thr Leu Ile Thr Thr Val
 20 25 30

gaa tcg aac tcg agt atg gac cta gga aaa ttc tgc ggg ctt tgt gtg 144
 Glu Ser Asn Ser Ser Met Asp Leu Gly Lys Phe Cys Gly Leu Cys Val
 35 40 45

tgt ccc tgt aac aag ctt aaa tcc agt gat gct tac aaa aaa gcc tgg 192
 Cys Pro Cys Asn Lys Leu Lys Ser Ser Asp Ala Tyr Lys Lys Ala Trp
 50 55 60

ggc aat aat cag gat gga gta gtg gcc agc cag cct gcc cgt gtg 240

Gly Asn Asn Gln Asp Gly Val Val Ala Ser Gln Pro Ala Arg Val Val	65	70	75	80	
gat gaa cgg gag cag atg gcc atc agt ggt ggc ttc atc cgc aga cgc					288
Asp Glu Arg Glu Gln Met Ala Ile Ser Gly Gly Phe Ile Arg Arg Arg					
	85		90		95
gtc taa					294
Val					

<210> 6
<211> 97
<212> PRT
<213> Artificial sequence

<220>
<223> Caspase 8 probe IETD SNAP-25(80-136)

<400> 6

Glu Gly Gly Gly Ser Ile Glu Thr Asp Ser Gly Gly Gly Ser	1	5	10	15	
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Gly Gly Gly Ser Phe Glu Pro Ser Glu Thr Leu Ile Thr Thr Val	20	25	30	
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Glu Ser Asn Ser Ser Met Asp Leu Gly Lys Phe Cys Gly Leu Cys Val	35	40	45	
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Cys Pro Cys Asn Lys Leu Lys Ser Ser Asp Ala Tyr Lys Lys Ala Trp	50	55	60	
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Gly Asn Asn Gln Asp Gly Val Val Ala Ser Gln Pro Ala Arg Val Val	65	70	75	80	
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Asp Glu Arg Glu Gln Met Ala Ile Ser Gly Gly Phe Ile Arg Arg Arg	85	90	95	
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Val

<210> 7
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<212> DNA
<213> Artificial sequence

<220>
<223> Caspase 3 probe DEVD-ANT-2

<220>
<221> CDS
<222> (1)..(957)

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gaa ggt gga gga ggt tca gat gaa gtc gat tca gga gga ggt gga tct					48
Glu Gly Gly Gly Ser Asp Glu Val Asp Ser Gly Gly Gly Ser	1	5	10	15	

gga ggt ggc gga tcc atg aca gat gcc gct gtg tcc ttc gcc aag gac					96
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Gly	Gly	Gly	Gly	Ser	Met	Thr	Asp	Ala	Ala	Val	Ser	Phe	Ala	Lys	Asp	
20								25					30			
ttc ttg gcc ggt gga gtg gcc gca gcc atc tcc aag aca gca gtc gta gca															144	
Phe	Leu	Ala	Gly	Gly	Val	Ala	Ala	Ile	Ser	Lys	Thr	Ala	Val	Ala		
35								40					45			
ccc atc gag agg gtc aag ctg ctg cag gtg cag cat gcc agc aag															192	
Pro	Ile	Glu	Arg	Val	Lys	Leu	Leu	Leu	Gln	Val	Gln	His	Ala	Ser	Lys	
50								55					60			
caa atc acg gca gat aag caa tac aag ggc atc ata gac tgc gtg gtt															240	
Gln	Ile	Thr	Ala	Asp	Lys	Gln	Tyr	Lys	Gly	Ile	Ile	Asp	Cys	Val	Val	
65								70					75		80	
cgt atc ccc aag gaa cag gga gtc ctg tcc ttc tgg cgt ggg aac ctg															288	
Arg	Ile	Pro	Lys	Glu	Gln	Gly	Val	Leu	Ser	Phe	Trp	Arg	Gly	Asn	Leu	
85								90					95			
gcc aat gtc atc aga tac ttc ccc acc cag gct ctc aac ttt gcc ttc															336	
Ala	Asn	Val	Ile	Arg	Tyr	Phe	Pro	Thr	Gln	Ala	Leu	Asn	Phe	Ala	Phe	
100								105					110			
aaa gat aaa tac aag cag atc ttt ctg ggt ggt gtg gac aag agg acc															384	
Lys	Asp	Lys	Tyr	Lys	Gln	Ile	Phe	Leu	Gly	Gly	Val	Asp	Lys	Arg	Thr	
115								120					125			
cag ttc tgg cgc tac ttt gca ggg aac ctg gca tca ggt ggt gcc gct															432	
Gln	Phe	Trp	Arg	Tyr	Phe	Ala	Gly	Asn	Leu	Ala	Ser	Gly	Gly	Ala	Ala	
130								135					140			
ggg gct aca tcc ttg tgc ttt gtg tac cct ctt gat ttt gcc cgt acc															480	
Gly	Ala	Thr	Ser	Leu	Cys	Phe	Val	Tyr	Pro	Leu	Asp	Phe	Ala	Arg	Thr	
145								150					155		160	
cgt cta gca gct gat gtg ggc aaa gct gga gct gaa agg gaa ttc aaa															528	
Arg	Leu	Ala	Ala	Asp	Val	Gly	Lys	Ala	Gly	Ala	Glu	Arg	Glu	Phe	Lys	
165								170					175			
ggc ctt ggt gac tgc ctg gtt aag atc tac aaa tct gat ggg att aag															576	
Gly	Leu	Gly	Asp	Cys	Leu	Val	Lys	Ile	Tyr	Lys	Ser	Asp	Gly	Ile	Lys	
180								185					190			
ggc ctg tac caa ggc ttt aat gtg tca gta cag ggc att atc atc tac															624	
Gly	Leu	Tyr	Gln	Gly	Phe	Asn	Val	Ser	Val	Gln	Gly	Ile	Ile	Ile	Tyr	
195								200					205			
cga gct gcc tac ttt ggt atc tat gac act gca aag gga atg ctc cca															672	
Arg	Ala	Ala	Tyr	Phe	Gly	Ile	Tyr	Asp	Thr	Ala	Lys	Gly	Met	Leu	Pro	
210								215					220			
gat ccc aag aat act cac atc ttc atc agc tgg atg att gca cag tct															720	
Asp	Pro	Lys	Asn	Thr	His	Ile	Phe	Ile	Ser	Trp	Met	Ile	Ala	Gln	Ser	
225								230					235		240	
gtc act gct gtc gct ggc ctg act tcc tat cct ttt gac acg gtt cgc															768	
Val	Thr	Ala	Val	Ala	Gly	Leu	Thr	Ser	Tyr	Pro	Phe	Asp	Thr	Val	Arg	
245								250					255			
cgt cgt atg atg cag tct gga cgc aaa gga act gat atc atg tac															816	
Arg	Arg	Met	Met	Met	Gln	Ser	Gly	Arg	Lys	Gly	Thr	Asp	Ile	Met	Tyr	

260

265

270

aca ggc acg ctt gac tgc tgg cg_g aag atc gc_g cgc gat gaa ggg agc
 Thr Gly Thr Leu Asp Cys Trp Arg Lys Ile Ala Arg Asp Glu Gly Ser
 275 280 285

aag gct ttt ttc aag ggc gca tgg tcc aac gtt ctc aga ggc atg ggt
 Lys Ala Phe Phe Lys Gly Ala Trp Ser Asn Val Leu Arg Gly Met Gly
 290 295 300

ggc gcc ttt gtg ctt gtc ttg tat gat gag atc aag aaa tac aca taa
 Gly Ala Phe Val Leu Val Leu Tyr Asp Glu Ile Lys Lys Tyr Thr
 305 310 315

<210> 8
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<220>
 <223> Caspase 3 probe DEVD-ANT-2

<400> 8

Glu Gly Gly Gly Ser Asp Glu Val Asp Ser Gly Gly Gly Ser
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Gly Gly Gly Ser Met Thr Asp Ala Ala Val Ser Phe Ala Lys Asp
 20 25 30

Phe Leu Ala Gly Gly Val Ala Ala Ala Ile Ser Lys Thr Ala Val Ala
 35 40 45

Pro Ile Glu Arg Val Lys Leu Leu Leu Gln Val Gln His Ala Ser Lys
 50 55 60

Gln Ile Thr Ala Asp Lys Gln Tyr Lys Gly Ile Ile Asp Cys Val Val
 65 70 75 80

Arg Ile Pro Lys Glu Gln Gly Val Leu Ser Phe Trp Arg Gly Asn Leu
 85 90 95

Ala Asn Val Ile Arg Tyr Phe Pro Thr Gln Ala Leu Asn Phe Ala Phe
 100 105 110

Lys Asp Lys Tyr Lys Gln Ile Phe Leu Gly Gly Val Asp Lys Arg Thr
 115 120 125

Gln Phe Trp Arg Tyr Phe Ala Gly Asn Leu Ala Ser Gly Gly Ala Ala
 130 135 140

Gly Ala Thr Ser Leu Cys Phe Val Tyr Pro Leu Asp Phe Ala Arg Thr
 145 150 155 160

Arg Leu Ala Ala Asp Val Gly Lys Ala Gly Ala Glu Arg Glu Phe Lys
 165 170 175

Gly Leu Gly Asp Cys Leu Val Lys Ile Tyr Lys Ser Asp Gly Ile Lys
 180 185 190

Gly Leu Tyr Gln Gly Phe Asn Val Ser Val Gln Gly Ile Ile Ile Tyr
 195 200 205
 Arg Ala Ala Tyr Phe Gly Ile Tyr Asp Thr Ala Lys Gly Met Leu Pro
 210 215 220
 Asp Pro Lys Asn Thr His Ile Phe Ile Ser Trp Met Ile Ala Gln Ser
 225 230 235 240
 Val Thr Ala Val Ala Gly Leu Thr Ser Tyr Pro Phe Asp Thr Val Arg
 245 250 255
 Arg Arg Met Met Gln Ser Gly Arg Lys Gly Thr Asp Ile Met Tyr
 260 265 270
 Thr Gly Thr Leu Asp Cys Trp Arg Lys Ile Ala Arg Asp Glu Gly Ser
 275 280 285
 Lys Ala Phe Phe Lys Gly Ala Trp Ser Asn Val Leu Arg Gly Met Gly
 290 295 300
 Gly Ala Phe Val Leu Val Leu Tyr Asp Glu Ile Lys Lys Tyr Thr
 305 310 315

<210> 9
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 <212> DNA
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<220>
 <223> Caspase 3 probe H2B-DEVD

<220>
 <221> CDS
 <222> (1)..(411)

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 aag gcg gtg act aag gcg cag aag aaa ggc ggc aag aag cgc aag cgc 96
 Lys Ala Val Thr Lys Ala Gln Lys Lys Gly Gly Lys Lys Arg Lys Arg
 20 25 30
 agc cgc aag gag agc tat tcc atc tat gtg tac aag gtt ctg aag cag 144
 Ser Arg Lys Glu Ser Tyr Ser Ile Tyr Val Tyr Lys Val Leu Lys Gln
 35 40 45
 gtc cac cct gac acc ggc att tcg tcc aag gcc atg ggc atc atg aat 192
 Val His Pro Asp Thr Gly Ile Ser Ser Lys Ala Met Gly Ile Met Asn
 50 55 60
 tcg ttt gtg aac gac att ttc gag cgc atc gca ggt gag gct tcc cgc 240
 Ser Phe Val Asn Asp Ile Phe Glu Arg Ile Ala Gly Glu Ala Ser Arg
 65 70 75 80
 ctg gcg cat tac aac aag cgc tcg acc atc acc tcc agg gag atc cag 288
 Leu Ala His Tyr Asn Lys Arg Ser Thr Ile Thr Ser Arg Glu Ile Gln
 85 90 95

acg gcc gtg cgc ctg ctg cct ggg gag ttg gcc aag cac gcc gtg 336
 Thr Ala Val Arg Leu Leu Leu Pro Gly Glu Leu Ala Lys His Ala Val
 100 105 110

tcc gag ggt act aag gcc atc acc aag tac acc agc gct aag gat cca 384
 Ser Glu Gly Thr Lys Ala Ile Thr Lys Tyr Thr Ser Ala Lys Asp Pro
 115 120 125

ccg gtc gat gaa gtc gat gcc acc atg 411
 Pro Val Asp Glu Val Asp Ala Thr Met
 130 135

<210> 10
 <211> 137
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Caspase 3 probe H2B-DEVD

<400> 10

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Lys Ala Val Thr Lys Ala Gln Lys Lys Gly Gly Lys Lys Arg Lys Arg 20 25 30

Ser Arg Lys Glu Ser Tyr Ser Ile Tyr Val Tyr Lys Val Leu Lys Gln 35 40 45

Val His Pro Asp Thr Gly Ile Ser Ser Lys Ala Met Gly Ile Met Asn 50 55 60

Ser Phe Val Asn Asp Ile Phe Glu Arg Ile Ala Gly Glu Ala Ser Arg 65 70 75 80

Leu Ala His Tyr Asn Lys Arg Ser Thr Ile Thr Ser Arg Glu Ile Gln 85 90 95

Thr Ala Val Arg Leu Leu Leu Pro Gly Glu Leu Ala Lys His Ala Val 100 105 110

Ser Glu Gly Thr Lys Ala Ile Thr Lys Tyr Thr Ser Ala Lys Asp Pro 115 120 125

Pro Val Asp Glu Val Asp Ala Thr Met
 130 135

<210> 11
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 <213> Artificial sequence

<220>
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<220>
<221> CDS
<222> (1)..(414)

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1 5 10 15

aag gcg gtg act aag gcg cag aag aaa ggc ggc aag aag cgc aag cgc 96
Lys Ala Val Thr Lys Ala Gln Lys Lys Gly Gly Lys Lys Arg Lys Arg
20 25 30

agc cgc aag gag agc tat tcc atc tat gtg tac aag gtt ctg aag cag 144
Ser Arg Lys Glu Ser Tyr Ser Ile Tyr Val Tyr Lys Val Leu Lys Gln
35 40 45

gtc cac cct gac acc ggc att tcg tcc aag gcc atg ggc atc atg aat 192
Val His Pro Asp Thr Gly Ile Ser Ser Lys Ala Met Gly Ile Met Asn
50 55 60

tcg ttt gtg aac gac att ttc gag cgc atc gca ggt gag gct tcc cgc 240
Ser Phe Val Asn Asp Ile Phe Glu Arg Ile Ala Gly Glu Ala Ser Arg
65 70 75 80

ctg gcg cat tac aac aag cgc tcg acc atc acc tcc agg gag atc cag 288
Leu Ala His Tyr Asn Lys Arg Ser Thr Ile Thr Ser Arg Glu Ile Gln
85 90 95

acg gcc gtg cgc ctg ctg cct ggg gag ttg gcc aag cac gcc gtg 336
Thr Ala Val Arg Leu Leu Pro Gly Glu Leu Ala Lys His Ala Val
100 105 110

tcc gag ggt act aag gcc atc acc aag tac acc agc gct aag gat cca 384
Ser Glu Gly Thr Lys Ala Ile Thr Lys Tyr Thr Ser Ala Lys Asp Pro
115 120 125

ccg gtc gtc gac gtc gcc gat gcc acc atg 414
Pro Val Val Asp Val Ala Asp Ala Thr Met
130 135

<210> 12
<211> 138
<212> PRT
<213> Artificial sequence

<220>
<223> Caspase 2 probe H2B-VDVAD

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Lys Ala Val Thr Lys Ala Gln Lys Lys Gly Gly Lys Lys Arg Lys Arg
20 25 30

Ser Arg Lys Glu Ser Tyr Ser Ile Tyr Val Tyr Lys Val Leu Lys Gln
35 40 45

Val His Pro Asp Thr Gly Ile Ser Ser Lys Ala Met Gly Ile Met Asn
 50 55 60

Ser Phe Val Asn Asp Ile Phe Glu Arg Ile Ala Gly Glu Ala Ser Arg
 65 70 75 80

Leu Ala His Tyr Asn Lys Arg Ser Thr Ile Thr Ser Arg Glu Ile Gln
 85 90 95

Thr Ala Val Arg Leu Leu Leu Pro Gly Glu Leu Ala Lys His Ala Val
 100 105 110

Ser Glu Gly Thr Lys Ala Ile Thr Lys Tyr Thr Ser Ala Lys Asp Pro
 115 120 125

Pro Val Val Asp Val Ala Asp Ala Thr Met
 130 135

<210> 13
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 <212> DNA
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<220>
 <223> Caspase 8 probe IETD-cb5RR

<220>
 <221> CDS
 <222> (1)..(174)

<400> 3
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 1 5 10 15

gga ggt ggc gga tcc ttc gag ccg tcc gaa act ctg atc act acc gtt 96
 Gly Gly Gly Ser Phe Glu Pro Ser Glu Thr Leu Ile Thr Thr Val
 20 25 30

gaa tcg aac tcg agt tgg tgg act aac tgg gtt atc cct gcg atc tct 144
 Glu Ser Asn Ser Ser Trp Trp Thr Asn Trp Val Ile Pro Ala Ile Ser
 35 40 45

gct ctg gtt gta gcg ctg atg tac cgg cgt taa 177
 Ala Leu Val Val Ala Leu Met Tyr Arg Arg
 50 55

<210> 14
 <211> 58
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Caspase 8 probe IETD-cb5RR

<400> 14

Glu Gly Gly Gly Ser Ile Glu Thr Asp Ser Gly Gly Gly Ser
 1 5 10 15

Gly Gly Gly Ser Phe Glu Pro Ser Glu Thr Leu Ile Thr Thr Val
20 25 30

Glu Ser Asn Ser Ser Trp Trp Thr Asn Trp Val Ile Pro Ala Ile Ser
35 40 45

Ala Leu Val Val Ala Leu Met Tyr Arg Arg
50 55